Claims

1. A method for identifying a nucleic acid encoding a fat metabolism regulator polypeptide whose inactivation results in an alteration in nematode fat content or localization, said method comprising:

(a) providing a mutagenized nematode;

(b) contacting said nematode with a dye that stains body fat; and

(c) comparing the body fat staining of said mutagenized nematode to a control nematode, wherein a mutation in a nucleic acid encoding a fat metabolism regulator polypeptide is identified by an alteration in nematode fat content or localization.

2. A method for identifying a nucleic acid that encodes a fat metabolism regulator polypeptide whose inactivation results in an alteration in nematode fat content or localization, said method comprising:

(a) contacting a nematode with a candidate inhibitory nucleic acid;

(b) contacting said nematode with a dye that stains body fat; and

(c) comparing the body fat staining of said nematode contacted with said inhibitory nucleic acid to a control nematode, wherein an alteration in body fat staining identifies the sense nucleic acid corresponding to said inhibitory nucleic acid, as a nucleic acid encoding a fat metabolism regulator polypeptide whose inactivation results in an alteration in nematode fat content or localization.

3. A method for identifying a candidate compound that modulates fat metabolism, said method comprising:

(a) providing a cell expressing a fat metabolism regulator nucleic acid selected from the group consisting of those encoding a polypeptide listed in Tables V, VI, VII, XII, XIII, or XIV;

(b) contacting said cell with a candidate compound; and

(c) comparing the expression of said nucleic acid in said cell contacted with said candidate compound with the expression of said nucleic acid in a control cell, wherein an

alteration in said expression identifies said candidate compound as a candidate compound that modulates fat metabolism.

4. The method of claim 3, wherein said cell is a nematode cell.

5. The method of claim 3, wherein said cell is a mammalian cell.

6. The method of claim 3, wherein said screening method identifies a compound that alters transcription or translation of said fat metabolism regulator nucleic acid.

7. The method of claim 3, wherein said cell is in a nematode.

8. The method of claim 3, wherein said fat metabolism regulator nucleic acids are selected from the group consisting of Tables V, VI, VII, XII, XIII, and XIV.

9. A method for identifying a candidate compound that modulates fat metabolism, said method comprising:

(a) providing a cell expressing a fat metabolism regulator polypeptide selected from the group consisting of those listed in Table V, VI, VII, XII, XIII, and XIV;

(b) contacting said cell with a candidate compound; and

(c) comparing the biological activity of said fat metabolism regulator polypeptide in said cell contacted with said candidate compound to a control cell, wherein an alteration in said biological activity of said fat metabolism regulator polypeptide identifies said candidate compound as a candidate compound that modulates fat metabolism.

10. A method for identifying a candidate compound that modulates fat metabolism, said method comprising:

(a) contacting a nematode with a candidate compound and a dye that stains body fat; and

(b) comparing staining by said dye in said nematode contacted with a candidate compound to a control nematode, wherein an alteration in said staining identifies said candidate compound as a candidate compound that modulates fat metabolism.

11. The method of claim 10, wherein said nematode comprises a mutation in a fat metabolism regulator nucleic acid molecule selected from the group consisting of *lpo-1*, *lpo-2*, *lpo-3*, *lpo-4*, *lpo-5*, *lpo-6*, and *lpo-7*.

12. A microarray consisting of at least two fat metabolism regulator nucleic acids or fragments thereof, wherein inactivation of each of said fat metabolism regulator nucleic acids results in an alteration in fat content of an organism compared to a control organism.

13. A microarray consisting of at least two of the fat metabolism regulator polypeptide molecules or fragments thereof, wherein inactivation of each of said fat metabolism regulator polypeptides results in an alteration in fat content of an organism compared to a control organism.

14. A method of identifying a candidate compound that modulates fat metabolism, said method comprising

a) contacting a cell with a candidate compound;

b) obtaining mRNA from said cell;

c) contacting a microarray of claim 12 with said mRNA; and

d) detecting an alteration in cellular mRNA levels of a fat metabolism regulator nucleic acid molecule in said cell contacted with said candidate compound compared to a control cell,; wherein said alteration identifies the candidate compound as a candidate compound that modulates fat metabolism.

15. A method of identifying a candidate compound that modulates fat metabolism, said method comprising the steps of

a) contacting a microarray of claim 13 with a candidate compound; and

b) detecting binding of said candidate compound to a fat metabolism regulator polypeptide, wherein said binding identifies the compound as a candidate compound that modulates fat metabolism.

16. A purified nucleic acid library, wherein at least 3% percent of the total nucleic acids in said library encode fat metabolism regulator polypeptides.

17. A method of identifying a candidate compound that modulates fat metabolism, said method comprising:

a) contacting a cell comprising one member of the library of claim 16; and

b) measuring the expression of the reporter gene; and

c) comparing the level of reporter gene expression in said cell contacted with said candidate compound with a control cell not contacted with said candidate compound, wherein an alteration in the level of the reporter gene expression identifies the candidate compound as a compound that modulates fat metabolism.

18. An isolated polypeptide comprising an amino acid sequence having at least 50% identity to the amino acid sequence of a polypeptide selected from the group consisting of those listed in Tables XV, XVI, and XVII, wherein expression of said polypeptide in an organism affects the regulation of fat metabolism in said organism.

19. The isolated polypeptide of claim 18, said polypeptide comprising the amino acid sequence of a polypeptide selected from the group consisting of those listed in Tables XV, XVI, and XVII.

20. An isolated nucleic acid molecule comprising a nucleotide sequence having at least 50% identity to the nucleotide sequence of a nucleic acid molecule selected from the group consisting of those that encode the polypeptides listed in Tables XV, XVI, and XVII, wherein expression of said nucleic acid molecule in an organism affects the regulation of fat metabolism in said organism.

21. A vector comprising the isolated nucleic acid molecule of claim 20.

22. A host cell comprising the vector of claim 21.

23. A transgenic animal expressing a fat metabolism regulator nucleic acid sequence, said nucleic acid sequence being selected from the group consisting of those that encode the polypeptides listed in Tables XV, XVI, and XVII.

24. An organism comprising a mutation in a fat metabolism regulator nucleic acid sequence said nucleic acid sequence being selected from the group consisting of those that encode the polypeptides listed in Tables XV, XVI, and XVII.

25. A double-stranded RNA corresponding to at least a portion of a fat metabolism regulator nucleic acid molecule of an organism said nucleic acid molecule being selected from the group consisting of those that encode the polypeptides listed in Tables XV, XVI, and XVII, wherein said double-stranded RNA is capable of decreasing the level of protein encoded by said fat metabolism regulator nucleic acid molecule.

26. An antisense nucleic acid molecule, wherein said antisense nucleic acid molecule is complementary to at least six nucleotides of a nucleic acid molecule selected from the group consisting of those that encode the polypeptides listed in Tables XV, XVI, and XVII, and wherein said antisense is capable of decreasing expression from the nucleic acid molecule to which it is complementary.

27. A method for diagnosing an organism having, or having a propensity to develop, a disease associated with fat metabolism regulation, obesity, or an obesity-related disease, said method comprising detecting an alteration in the sequence or expression of a fat metabolism regulator nucleic acid molecule relations to the wild-type sequence, said fat metabolism regulator

nucleic acid molecule being selected from the group consisting of those that encode the polypeptides listed in Tables XII, XIII, and XIV.

28. A method for diagnosing an organism having, or having a propensity to develop, a disease associated with fat metabolism regulation, obesity, or an obesity-related disease, said method comprising detecting an alteration in the biological activity of a fat metabolism regulator polypeptide relative to the wild-type level of activity.

29. A collection of primer sets, each of said primer sets comprising at least two primers that bind to a fat metabolism regulator nucleic acid molecule that encodes a polypeptide selected from the group consisting of those listed in Tables IX, X, XI, XII, XIII, and IV under high stringency conditions, said collection comprising at least two primer sets.